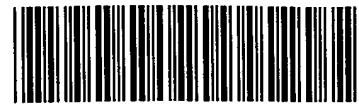


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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/025,145A

DATE: 07/23/2002
TIME: 15:54:32

Input Set : A:\WSUR18414Seq2.txt
Output Set: N:\CRF3\07232002\J025145A.raw

3 <110> APPLICANT: Croteau, Rodney B.
 4 Bohlmann, Joerg
 5 Steele, Christopher L.
 6 Phillips, Michael A.
 8 <120> TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
 10 <130> FILE REFERENCE: WSUR118414
 12 <140> CURRENT APPLICATION NUMBER: 10/025,145A
 C--> 13 <141> CURRENT FILING DATE: 2002-06-28
 15 <150> PRIOR APPLICATION NUMBER: US 09/360,545
 16 <151> PRIOR FILING DATE: 1999-07-26
 18 <150> PRIOR APPLICATION NUMBER: PCT/US98/14528
 19 <151> PRIOR FILING DATE: 1998-07-10
 21 <150> PRIOR APPLICATION NUMBER: US 60/052,249
 22 <151> PRIOR FILING DATE: 1997-07-11
 24 <160> NUMBER OF SEQ ID NOS: 107
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 29 <211> LENGTH: 2196
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Abies Grandis
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (69)..(1952)
 36 <223> OTHER INFORMATION:
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 43 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
 44 1 5 10
 46 ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
 47 Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
 48 15 20 25 30
 50 aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
 51 Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
 52 35 40 45
 54 cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
 55 Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
 56 50 55 60
 58 caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
 59 Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
 60 65 70 75
 62 ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350
 63 Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg

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67	Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr			
68	95	100	105	110
70	ctg gat gat gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc			446
71	Leu Asp Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg			
72	115	120	125	
74	ctt tgg ata gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc			494
75	Leu Trp Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe			
76	130	135	140	
78	aag aac gag ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag			542
79	Lys Asn Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu			
80	145	150	155	
82	gaa aac ggc att gga tgt ggg aga gac agt att gtt act gat ctc aac			590
83	Glu Asn Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn			
84	160	165	170	
86	tca act gcg ttg ggg ttt cga act ctt cga tta cac ggg tac act gta			638
87	Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val			
88	175	180	185	190
90	tct cca gag gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta			686
91	Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val			
92	195	200	205	
94	tgc tcc ccc ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta			734
95	Cys Ser Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu			
96	210	215	220	
98	tat cgg gct tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa			782
99	Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu			
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102	gct gaa atc ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att			830
103	Ala Glu Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile			
104	240	245	250	
106	cca gtc tcc gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc			878
107	Pro Val Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly			
108	255	260	265	270
110	tgg cac aca aat ttg cca aga ttg gaa gca aga aat tac ata gac aca			926
111	Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr			
112	275	280	285	
114	ctt gag aaa gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag			974
115	Leu Glu Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys			
116	290	295	300	
118	ctt tta gaa ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa			1022
119	Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln			
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122	caa aag gaa tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg			1070
123	Gln Lys Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu			
124	320	325	330	
126	cct aaa ttg aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg			1118
127	Pro Lys Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu			
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131	Ala	Ser	Cys	Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	
132					355					360					365		
134	ttc	gcc	aaa	atg	tgt	cat	ctt	gtc	aca	gtt	ttg	gac	gat	att	tac	gac	1214
135	Phe	Ala	Lys	Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	
136					370					375					380		
138	act	ttt	gga	acg	att	gac	gag	ctt	gaa	ctc	ttc	aca	tct	gca	att	aag	1262
139	Thr	Phe	Gly	Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	
140		385				390					395						
142	aga	tgg	aat	tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	1310
143	Arg	Trp	Asn	Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	
144		400				405					410						
146	gtg	tac	atg	gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcg	1358
147	Val	Tyr	Met	Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	
148	415				420					425					430		
150	gag	aag	act	caa	ggg	aga	aac	act	ctc	aac	tat	gtt	cga	aag	gct	tgg	1406
151	Glu	Lys	Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	
152		435				440					445						
154	gag	gct	tat	ttt	gat	tca	tat	atg	gaa	gca	aaa	tgg	atc	tct	aat		1454
155	Glu	Ala	Tyr	Phe	Asp	Ser	Tyr	Met	Glu	Glu	Ala	Lys	Trp	Ile	Ser	Asn	
156		450				455					460						
158	ggt	tat	ctg	cca	atg	ttt	gaa	gag	tac	cat	gag	aat	ggg	aaa	gtg	agc	1502
159	Gly	Tyr	Leu	Pro	Met	Phe	Glu	Glu	Tyr	His	Glu	Asn	Gly	Lys	Val	Ser	
160		465				470					475						
162	tct	gca	tat	cgc	gta	gca	aca	ttg	caa	ccc	atc	ctc	act	ttg	aat	gca	1550
163	Ser	Ala	Tyr	Arg	Val	Ala	Thr	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asn	Ala	
164		480				485					490						
166	tgg	ttt	cct	gat	tac	atc	ttg	aag	gga	att	gat	ttt	cca	tcc	agg	ttc	1598
167	Trp	Leu	Pro	Asp	Tyr	Ile	Leu	Lys	Gly	Ile	Asp	Phe	Pro	Ser	Arg	Phe	
168	495					500					505					510	
170	aat	gat	ttg	gca	tcg	tcc	ttc	ctt	cg	cta	cga	ggt	gac	aca	cgc	tgc	1646
171	Asn	Asp	Leu	Ala	Ser	Ser	Phe	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	
172		515				520					525						
174	tac	aag	gcc	gat	agg	gat	cgt	ggt	gaa	gaa	gct	tcg	tgt	ata	tca	tgt	1694
175	Tyr	Lys	Ala	Asp	Arg	Asp	Arg	Gly	Glu	Glu	Ala	Ser	Cys	Ile	Ser	Cys	
176		530				535					540						
178	tat	atg	aaa	gac	aat	cct	gga	tca	acc	gaa	gaa	gat	gcc	ctc	aat	cat	1742
179	Tyr	Met	Lys	Asp	Asn	Pro	Gly	Ser	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	
180		545				550					555						
182	atc	aat	gcc	atg	gtc	aat	gac	ata	atc	aaa	gaa	tta	aat	tgg	gaa	ctt	1790
183	Ile	Asn	Ala	Met	Val	Asn	Asp	Ile	Ile	Lys	Glu	Leu	Asn	Trp	Glu	Leu	
184		560				565					570						
186	cta	aga	tcc	aac	gac	aat	att	cca	atg	ctg	gcc	aag	aaa	cat	gct	ttt	1838
187	Leu	Arg	Ser	Asn	Asp	Asn	Ile	Pro	Met	Leu	Ala	Lys	Lys	His	Ala	Phe	
188	575					580					585					590	
190	gac	ata	aca	aga	gct	ctc	cac	cat	ctc	tac	ata	tat	cga	gat	ggc	ttt	1886
191	Asp	Ile	Thr	Arg	Ala	Leu	His	His	Leu	Tyr	Ile	Tyr	Arg	Asp	Gly	Phe	
192		595				600					605						
194	agt	gtt	gcc	aac	aag	gaa	aca	aaa	aaa	ttg	gtt	atg	gaa	aca	ctc	ttt	1934

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198	gaa	tct	atg	ctt	ttt	taa	ctataaccat	atccataata	ataagctcat						1982	
199	Glu	Ser	Met	Leu	Phe											
200				625												
202	aatgctaaat	tattggcctt	atgacatagt	ttatgtatgt	acttgtgtga	attcaatcat									2042	
204	atcggtgtggg	tatgattaaa	aagctagagc	ttacttaggtt	agtaaacatgg	tgataaaaagt									2102	
206	tataaaaatgt	gagttataga	gatacccatg	ttgaataatg	aattacaaaa	agagaaaattt									2162	
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219	1				5				10						15	
222	Lys	Ser	Leu	Ile	Ser	Ser	Ile	His	Glu	His	Lys	Pro	Pro	Tyr	Arg	Thr
223						20			25						30	
226	Ile	Pro	Asn	Leu	Gly	Met	Arg	Arg	Arg	Gly	Lys	Ser	Val	Thr	Pro	Ser
227						35			40						45	
230	Met	Ser	Ile	Ser	Leu	Ala	Thr	Ala	Ala	Pro	Asp	Asp	Gly	Val	Gln	Arg
231						50			55						60	
234	Arg	Ile	Gly	Asp	Tyr	His	Ser	Asn	Ile	Trp	Asp	Asp	Asp	Phe	Ile	Gln
235	65						70			75					80	
238	Ser	Leu	Ser	Thr	Pro	Tyr	Gly	Glu	Pro	Ser	Tyr	Gln	Glu	Arg	Ala	Glu
239							85			90					95	
242	Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	Leu	Asp
243						100			105						110	
246	Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	Leu	Trp
247						115			120						125	
250	Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	Lys	Asn
251						130			135						140	
254	Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	Glu	Asn
255	145						150			155					160	
258	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	Ser	Thr
259						165			170						175	
262	Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	Ser	Pro
263						180			185						190	
266	Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser
267						195			200						205	
270	Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg
271						210			215						220	
274	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Ala	Glu	
275	225						230			235					240	
278	Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val
279							245			250					255	
282	Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His
283						260			265						270	
286	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu

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294	Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys		
295	305	310	315
298	Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys		
299	325	330	335
302	Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser		
303	340	345	350
306	Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala		
307	355	360	365
310	Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe		
311	370	375	380
314	Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp		
315	385	390	395
318	Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr		
319	405	410	415
322	Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys		
323	420	425	430
326	Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala		
327	435	440	445
330	Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr		
331	450	455	460
334	Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala		
335	465	470	475
338	Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu		
339	485	490	495
342	Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp		
343	500	505	510
346	Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys		
347	515	520	525
350	Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met		
351	530	535	540
354	Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn		
355	545	550	555
358	560	565	570
359	575	580	585
362	Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile		
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366	605	600	605
367	610	615	620
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Output Set: N:\CRF3\07232002\J025145A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:8; N Pos. 6,12
Seq#:9; N Pos. 3,6,9,12
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Seq#:14; N Pos. 93
Seq#:21; N Pos. 3,12
Seq#:22; N Pos. 6,12,15,18
Seq#:23; N Pos. 7,10,16
Seq#:25; Xaa Pos. 3,4,6,8
Seq#:26; Xaa Pos. 3,4,6
Seq#:27; Xaa Pos. 2,3,4
Seq#:28; Xaa Pos. 6
Seq#:45; Xaa Pos. 3,4
Seq#:46; Xaa Pos. 4
Seq#:50; Xaa Pos. 1
Seq#:51; Xaa Pos. 1
Seq#:52; Xaa Pos. 1
Seq#:53; Xaa Pos. 6
Seq#:56; N Pos. 1,4,7